```
OM of: US-09-525-998A-1 to: SPTREMBL_17:*   out_format = pfs

Date: Apr 23, 2002 10:34 PM

About: Results were produced by the GenCore software, version 4.5.
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
 -MODEL=frame+_n2p.model -DEV=xlp
 -QUERY=...rspt  -SPT=....  ...;..;....4.....;.;.4/;4q -query:fasta+.....;
 -DB=SPTREMBL_17 -QFMT=fastan -SUFFIX=rspt -GAPOP=12.000
 -GAPEXI=4.000 -MINMATCH=0.100 -YGAPEXT=0.000 -YGAPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
 -QGAPOP=6.000 -XGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
 -TRANS=human40.cdi -ITST=45 -DWCNTICN=200 -THR_SCORE=pct
 -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pls
 -NORM=EXT -MINLEN=0 -MAXLEN=2000000000
 -USER=US09525998 -QCN1_1=186 -NCN1=6 -ICN1=3 -ICNTICG -NO_XLPXY
 -WAIT -THREADS=1

Search information block:
Query: US-09-525-998A-1
Query length: 1368
Database: SPTREMBL_17:*
Database sequences: 473505
Database length: 146272329
Search time (sec): 178.700000
```

```
score_list:
Sequence                      Strd  Orig     ZScore    EScore    Len !  Documentation
sp_mammal:Q97530                +    873.00   1126.06   9.9e-55   189 !  Q97530 canis familiaris (dog)
sp_mammal:Q95185                +    866.00   1117.04   1.2e-54   189 !  Q95185 felis silvestris catus  c
sp_mammal:Q99MM1                +    383.00   484.85    3.1e-19   418 !  Q99MM1 mus musculus (mouse).  ws
sp_human:C00275                 +    377.50   482.59    3.1e-19   417 !  O00275 homo sapiens (human).  ly
sp_human:Q9AV86                 +    372.00   475.10    7.7e-19   417 !  Q9AV86 homo sapiens (human).  de
sp_human:O14865                 +    362.50   463.24    3.7e-18   426 !  O14865 homo sapiens (human).  de
sp_human:O00280                 +    354.50   453.61    1.4e-17   490 !  O00280 homo sapiens (human).  ly
sp_human:O90274                 +    344.50   440.12    4.8e-17   490 !  O90274 homo sapiens (human).  ly
sp_vertebrate:Q9PVM4            +    233.00   294.89    4.0e-09   387 !  Q9PVM4 xenopus laevis (african
sp_rodent:Q99MW1                +    230.00   292.58    7.2e-09   417 !  Q99MW1 mus musculus (mouse).  50
sp_vertebrate:Q87408            +    227.50   290.00    1.4e-08   468 !  Q87408 meleagris gallopavo.  50
sp_vertebrate:Q9DFV0            +    225.00   285.84    2.7e-08   438 !  Q9DFV0 brachydanio rerio (zebra
sp_human:O14866                 +    219.50   281.46    7.5e-08   277 !  O14866 homo sapiens (human).  sc
sp_human:O15531                 +    217.50   276.15    4.0e-08   440 !  O15531 homo sapiens (human).  af
sp_human:O14763                 +    215.00   272.93    4.0e-07   440 !  O14763 homo sapiens (human).  ap
sp_human:Q9HVE0                 +    215.00   272.19    4.0e-07   440 !  Q9HVE0 homo sapiens (human).  tu
sp_human:Q9Z2M4                 +    214.00   272.19    1.7e-07   381 !  Q9Z2M4 mus musculus (mouse).  k1
sp_human:O15517                 +    213.00   270.75    2.0e-07   411 !  O15517 homo sapiens (human).  cy
sp_rodent:Q9JJL6                +    212.00   269.91    2.4e-07   384 !  Q9JJL6 mus musculus (mouse).  cy
sp_vertebrate:Q9DF34            +    211.00   269.00    2.9e-07   357 !  Q9DF34 brachydanio rerio (zebra
sp_human:O14720                 +    210.50   247.53    3.0e-07   411 !  O14720 homo sapiens (human).  dc
sp_human:O15508                 +    210.50   247.53    3.0e-07   253 !  O15508 homo sapiens (human).  ps
sp_human:O00276                 +    209.00   247.17    5.1e-07   259 !  O00276 homo sapiens (human).  ly
sp_rodent:O63327                +    204.50   258.14    7.2e-07   459 !  O63327 mus musculus (mouse).  t
sp_human:O16042                 +    204.00   258.05    8.8e-07   425 !  O16042 homo sapiens (human).  tu
sp_human:Q9UME5                 +    203.50   261.65    2.6e-06   175 !  Q9UME5 homo sapiens (human).  d
sp_human:Q9UMF0                 +    203.50   263.44    1.2e-06   178 !  Q9UMF0 homo sapiens (human).  ly
sp_human:Q9UMF1                 +    203.50   263.41    1.2e-06   181 !  Q9UMF1 homo sapiens (human).  ly
sp_human:O88734                 +    203.50   257.57    9.3e-07   482 !  O88734 mus musculus (mouse).  p8
sp_rodent:Q9Z2A4                +    201.50   258.80    1.6e-06   180 !  Q9Z2A4 mus musculus (mouse).  28
sp_rodent:Q9ER63                +    200.50   260.71    2.6e-06   147 !  Q9ER63 mus musculus domesticus.
sp_human:O00228                 +    200.50   247.87    1.8e-06   468 !  O00228 homo sapiens (human).  cy
sp_vertebrate:Q9AR7             +    199.50   254.00    1.9e-06   468 !  Q91AR7 gallus gallus (chicken)
sp_rodent:Q99R62                +    198.50   258.38    2.9e-06   111 !  Q99R62 mus musculus domesticus
sp_rodent:Q9JJL5                +    196.00   244.22    3.4e-06   385 !  Q9JJL5 mus musculus (mouse).  tr
sp_human:O00278                 +    195.00   259.87    4.5e-06   234 !  O00278 homo sapiens (human).  ly
sp_rodent:Q9DCQ1                +    191.50   244.39    7.4e-06   327 !  Q9DCQ1 mus musculus (mouse).  ly
sp_mammal:Q9XS20                +    189.00   241.94    1.0e-05   329 !  Q9XS20 oryctolagus cuniculus (r
sp_vertebrate:Q9PW79            +    189.00   241.11    1.0e-05   268 !  Q9PW79 gallus gallus (chicken)
sp_mammal:Q91V79                +    189.00   241.31    1.0e-05   319 !  Q91V79 oryctolagus cuniculus (r
```

```
seq_name: sp_mammal:Q97530

seq_documentation block:
ID   Q97530        .....;MINMAL.         IT:   189 AA.
AC   Q97530;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR F60 (FRAGMENT).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Caridae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Duthie S., Nasir L., Argyle D.J., Eckersall P.D.;
RT   "Canine tumor necrosis factor receptor, partial cds.";
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF013955; AAD01516.1; -.
DR   HSSP; P19438; 1TNR.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 3.
DP   PROSITE; PS01186; EGF_2; UNKNOWN 1.
DP   PROSITE; PS00652; TNFR_NGFR_1; 3.
DP   PROSITE; PS00050; TNFR_NGFR_2; 2.
KW   Receptor.
FT   NON_TER        189
SQ   SEQUENCE   189 AA;   21324 MW;  5DFA6FA567...... CRC64;
```

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alignment_block:
     Quality:    873.00           Length:    188
     Ratio:       5.105           Gaps:       0
Percent Similarity:  35.952      Percent Identity:  31.915

alignment_block:
US-09-525-998A-1 x Q97530

Align Seq 1/1 to: Q97530   from 1   to: 189

  1 ATGGGCTTCTCACGGGCCGTGCCCACCTGTGGTGCCATAGTGTCCTCGGA  50
    |||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetGlyLeuProThrValProGlyLeuLeuLeuProLeuValLeuLeuAl  17

 51 GCTGGTGGGAGAAGAAATATCCGGGCAGGGTATGGACAGCAGCGTGACAGC  100
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 17 AlaLeuProGluGlyIleGlyValIleAlaValProHisSer  34

101 TAGGGCAGAGAAGAAAGAAGAGCAGGTGTGCAAAGAAAATATATC  150
    ||||||||||||||||||||||||||||||||||||||||||||||
 34 ArgAlaGluLysLysGluGluGlnValCysLysGluAsnIlc  50

151 CAAGTTAAAATAATTGGATTTAGAAGTGCAAATGCAGAAGCAGAA  200
    ||||||||||||||||||||||||||||||||||||||||||||||
 51 HisLeuLysAspAspSerIleCysCysLysCysGlnLysGlyThr  67

201 GTGGAGAAGAAAGAAGGTATAGGGCATAGCAGGAGAA  250
    ||||||||||||||||||||||||||||||||||||||
 67 ValGluLysLysGluGlyIleGlyHisSerArgArgGlu  84

251 GTGAAATGGTGTTTCACTGGTTTGAAAAGAGGCAGTTAGATGCTGTC  300
    |||||||||||||||||||||||||||||||||||||||||||||
 84 ValLysTrpCysPheThrAlaLeuLysArgAlaAspAlaValCys  100
```

Left column:

```
301 AGTGTCCAAATGCGAAAGGAATGGGTCAGGTGGAGATCTCTTTG 350
    |||||  ||||||||||||||||||||||||||||||||||||||
101 SerCysSerLysArgLysSArgLysCysSValGluIleSerProCy 117

351 CACAGTGGACGGACGGACACCGTGTGGCTGCAGGAAGAACCAGTACCGGC 400
    |||||||   |||||||||||||||||||||||||||||||||||||
117 sThrValTyrArgAspThrValCysGlyCysSArgLysAsnGlnTyrArgP 134

401 ATTATTGGAGTCAAAACCTTTCCAGTGCTTCAATTGCAGCCTCTGCCTC 450
    |||||||||  |||||||||||||||||||||||||||||||||||||
134 heTyrTrpSerGluThrLeuPheGlnCysPheGlnCysAsnAsnCysSerLeu 150

451 AATGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCAC 500
    ||||||||||||||||||||||||||||  |||||||||||||||||||
151 AsnGlyThrValCysIleSerProCysGlnGluLysGlnAsnThrIleCysSh 167

501 CTGCGCATGCAGSTTCTGTCGAAGAGAAAGAGTGTCCTGTAGTA 550
    |||||||||||||  |||||||||||||||||||||||||||||
167 rCysHisAlaGlyPhePheLeuArgGluHisGluArgValGluIleSerProCy 184

551 ACTGTAAGAAAAGC 564
    ||||||||||:::
184 snCysLysLysAsn 188
```

seq_name: sp_mammal:Q95185

alignment_scores:
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        Quality:  866.00            Length:   188
        Ratio:      5.186           Gaps:       0
Percent Similarity: 88.830      Percent Identity: 82.447
```

alignment_block:
US-09-525-998A-1 x Q95185

Align seq 1/1 to: Q95185 from 1 to 189

```
  1 ATGGGCCTCTCACAAATGCCTGCAGTCTGTCTGGCANTGGTGCTCCTGGA 50
    ||||||| |||||||||||||||||| ||||||    |||||||||||||
  1 MetGlyLeuSerGlnMetProAlaValCysLeuLeuProValLeuLeuAl 17

 51 GCTGTGGTGGAAIAIANCCTCAGGGTTCATTGATTGGANTGGTANTAGC 100
    |||||||| ||  ||||||  || ||||||  |||  |||||||||||||
```

alignment block:
US-09-525-998A-1 x Q99MM1

Align seq 1/1 to: Q99MM1 from: 1 to: 413

```
 25 CTGCTGCTGCCACTGGTGCTGCTCGGAGCGTGTTGGTGGGAAATATACCCCTC  74
    !!!!!!!!  !!! !!!!!!!!! !!!!!! !!!    !!!!!!!
 18 LeuLeuLeuLeuLeuLeuLeuLeuLeuLeuGlyGlnGlyGlnGlyGlnGlI  34

 75 AGGGTTATTGGATGGTCCTACTAGGGACAGGAGAGAGAGATA 124
    !!!!!!  !!!       !!:  ::!!!!!
 34 yGlyMetSerGlyArgCysAspCysAlaSerGlnLysArg....  49

125 GTGTGTGTCCCAAGGAAAATATCACCTCAAAATAATCGATTTGC 174
    ::: :!!!!!!!         ::!!!!!
 50 ...........TyrGlyProPheCys  54

175 TGTACCAAGTGCCACAAAGGAACCTACTTGTACAATCACTGTCCAGGCCCC 224
    !!!!!!! !!!  !!!!!! !!!     !! 
 55 CysArgGlyCysProCysLysGlyHisTyrMetLysAlaProCysAlaGluPr  71

225 GGGCGAGAATAACCACTGGAGAGGAGAGAGGCTCTTCAAGGCTT 274
    :::::!!!!!!! !!!!!
 71 oCysGlyAsnSerThrCysLeuProCysProSerAspThrPheLeuThrA  88

275 CAGAAAGCCAGTCAGA     CATGCTTAGTGTTCCAAATATGGAAAG 321
    :!!!!!!!!!!!:::    !!! !!!!! ::: !!!!!!!
 88 rgAspAsnHisPheLysThrArgCysThrArgCysGlnValCysSerAspGlu 104

322 GAAAATGGGTGCAGTGGACATGTTCTTGTGCAGTGGAGACACCGGT 371
    :!!!!!!!!!!!   !!!!! !!!    !!!!!!!
105 GluAlaLeuGlnValThrLeuGluAsnCysSerAlaLysSerAspThrHi 121

372 GTGTGGTTGTAAGGAGGATATTATTGGAGTGAAAACCTTT 421
    ::!!!!!!!    !!!!!!
121 sCysGlyCysGlnSerGly..........Trp  128

422 TCCAGTGGTTCAATTGAGTGTTGGTTCAATTGGA  . 457
    !!! !!!!!!  !!!
129 ....CysValAspCysSer ThrValProCysGlyLysSerSerProPh 143

458 .......CGGTGC.....ACCTCTGCCAGGAGAGAAACAGAAACAC 491
    ::! !!!!:::!!!!!!!    !!!!!!
143 eSerCysValProCysGlyAlaThrThrProValHisGluAlaProThrP 160

492 CGTGTGCATGCCATGCAGGTTCTTCTTCTAAGAGAAACGAAGTGTGTCT 541
    !!! !!! !!!:::!!!!!!!! !!:::!!!
160 ro..ArgProCysLeuProCysProGlyThrCysArgCysAsnAspCysThrS 176

542 CCTGT...........AGTAACTGTAAGAAAAGCCTGGAGTGCACG 576
    !!!!!   !!!!! !!!!!!
176 erCysProThrGlyPheSerProValCysProLysAla.......CysThr 190

577 AAGTTGTGCCTACCCAGCAATGCAGAATCTTCAAGCCGACTGCAGGCGACTCA 624
    ::!!!!!  :::!!!!!!!!  !!!!!!!
191 AlaValCys  GlyTrpTyrLysGlnMetPh 199

625 .GGCACCAGAGTGCTGTGGCGTGCCGTCAATTTCTTGGTCTTGGCCTTT 673
    ::: :!!!!!!!!  ::::!!!!!!!  !!!!!!!
199 erTrpValGlnValLeuGluGlyValAlaAlaProLeuProProGlyTyrAlaLeuGlu 216

674 TATCCCTCCTCTTCATTGGTTAAGTGATGGTACCAAGTGGGAGTCC 723
    !!  !!!!!!!!! :::!!!!!!!!!
216 leCys.............AlaTyrCysArgTrpGlu.......... 223

724 AAGCCTACTCACCATGTTGTGGGAAATATCGACTACCTGCAAAAAGAGAGGGGGA 773
    :::!!!!!!!    !!!!!!
224 ProCysLysAlaValVal............ThrAlaAspThrAlaGly.. 235

774 GCTTGAAGGAACTACTAGCCCCTGGCC...CCAAAACCCAAGCTTCA 820
    ::!!!!!!!   !!!:::   !!!
236 .......ThrGluProLeuAlaSerProCysThrProAlaHis...  247
```

```
821 GTCCCAGTCCAGGGTCAGCCCCACGGTCATCCATGGTCCATGGGAACGGGTTCAATGGTTCAGT 870
    !!!!!!!!   !!!!!!!                !!!!!!!   :::!!!
247 euSerAlaSerAspSerAlaHisThrLeu..LeuAlaPro..ProSer 261

871 TCCACTTCACCCCCAGTGCCAC.......................... TATAT 893
    !!!:!          !!!!!!
262 ..SerThrGlyProSerAlaValThrValThrProCysVa..CysAspAspThriH 278

900 CCCGGTACTGAGCCACATTTGAGCTCCCCGGAGAAGAGGTGGTACCAG 949
    !!!!!!!!  ::: !!!!!!!!
278 rProGlyThrGluSerHisGlnSerProValValGlnValHisAlaSerProGlu 295

950 CCTAT...CAGGGGCTCAGCCCCATCCTGCAGCAGCCCTGGAAACTGCAAGAC 996
    ::!!!!!!       !!!!!!!       !!!!!!!
295 rGThrProAspGlnGlyLeuProAsnArgThrLeuGlyThrProLeuAlaSerPro 311

997 CCCAGCCCAAAGCTTCAGAAAGAGGAAGAGATAAAGGTGAAACATCGAAGCATA 1046
    !!!!!!! !!!!!!!               !!!!!!!
312 LeuSerProAlaPro.............ProAlaGlySerProAl 322

1047 GAGCGGTCAGACTGCATGAGCCCGGTGAGCGTGTAGGGCGGTGGTGGAGAACG 1096
     !!!!!!!!  :::!!!!!!!!
322 aAlaValLeuGluThrProGlyPro..GlnLeuCysValMetAspAspAlaV 338

1047 TGGCCCCGGTTGCGGTGGAGGAATTCGTCGGGGCGGCTAGGGTGGAGGGAC 1146
     !!!!!!!!!!!!!!!  :::!!!!!!!!!!
338 alProAlaArgAtArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 354

1147 CACGAGAT ATGCCGCAGCTCAGAACGGCGTCGTCCTCGGGGAGTGC 1146
     !!!!!!! !!!!!!!    !!:::
355 AlaGluHisGlnGluAlaValGluValGluIleCysArg...PheArgAspGlu 370

1197 GCAATACAGCCATGTTGGCGGACCTGGAGCGGCGGACGCGGGAGGAGGAGG 1246
     !!!!!!!!!  !!! !!!
370 nGlnIleTyrGlnMetLeuLysArgIrpArgGlnGlnArgPro........A 384

1247 CCAGCTGGACTTGCTGGGAGCGGCTGGGAAGCGGACCTGGTGGAGGGL 1296
     !!! !!!    !!! !!!
384 laGlyLeuGlyAlaIleTyrAlaAlaGlnAlaGlyArgGlySerGlyArgGlyGly 400

1297 TGCCTGGAGGACACGAGGAGGGGCTT 1323
     !!!
401 CysAlaGluGluAspArgArgSerArgGluLeu 409
```

seq_name: sp_human:O00275

seq_documentation block:

DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00298; TNFR; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS00652; TNFR_NGFR_1; ?.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ   SEQUENCE   418 AA; 45456 MW; 54B48F8B35C629E2 CRC64.

alignment_scores:
           Quality: 377.50   Length: 463
           Ratio: 1.641   Gaps: 23
Percent Similarity: 49.676   Percent Identity: 28.726

alignment_block:
US-09-525-998A-1 x 000275

Align seq 1/1 to: 000275   from: 1 to: 418

 43 CTCCTGGAGTCTTGTGGAAATATCCCTCAGGGGTTATTGGACTGT 92
          ||||| :|:|||:|| :|||:|
 15 LeuLeuGluValCysGlyAlaArgAlaIleGly............ 26

 93 CCCTCACCTAGGGAGCAGGGAGAGAGAATATGTGTCCCAAGGAA 142
          ||| |||:||| ||| ||:
 27 ......GlyThrArgSerProArg   CysAspCysAlaG 37

143 AATATATCCACCCTCAAAATAATTCGATTGCTGCCAAGTGCCACAAA 192
          |||||||| ::||||||| |:||:||| ||
 37 LysAspPheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAla 53

193 GGAACTACTGTATAATGATGTTCCCAACCAAGTAGGAATAAGGACTG 242
          ||: ||| ||:||:|| |||::|| |||:||| |||||
 54 GlyHisTyrLeuLysLysAlaProCysThrGluProCysGlyAsnSerThrCy 70

243 CAGGAAGTGTTAGAGTTCTTTCACACCATTCAAAACCACTTAGA 291
          |||| |:: :||:| |||||: |||||||
 70 sLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHisHisAsnS 87

292 ..CACTGCCTCAGCTGCTCCAAATGCCGAAAGCAAATGGGTCAGCTGGAG 339
          | ||||| ||||| ::||||||| :||||||||
 87 erGlyCysAlaArgCysGlnAlaCysAspGluGluAlaSerGlnValAla 103

340 ATCTCTTCTTGCCACAGTGAATGGAACACTGGTGATGTTGTAAGAA 389
          ::|::|||| |||| ::|:|||:||||| :|:|||||
104 IleSerSerCysAlaValAlaAspGluArgCysGlyCysProGl 120

390 CCAGTACGGATATTATTGGATGAAACTTTCCAGTGC 429
          ||| ::| :|||| ||||| |||||
120 yThrPheValGluCys.........GlnValSerGlnCysValSerSerS 134

430 ..TTCAATTGCAGCCCTCCGCTCAAT..CGGACCGGCCAC 465
          :||| |||||| |||||| :|||||||
134 erProPheTyrCysSerLeuAspCysGlyAlaLeuHisArgHis 150

466 ......CCTCCTGCCAGGAGAAACAGAACAGGGTGCACCTGCATGC 509
          ||| |||||:|||:|| ||||||||||
151 ThrArgGluLeuCysSerCysArgArgAspThrArgCysLeuCysPr 167

510 AAGTTTCTTTCTTCTAAGAAAAACGAGTGTGTCTCCTGT......... 546
          ::||||||||||||||
167 sGlyPheTyrGluHisGlyArgGlyCysValSerCysProThrSerThrL 184

547 .AGTAACTTGTAAGAAAAGCCTTGAGTTCAGGAGCTTACCCCAG 594
          :||||||||||| |||||
184 euGlySerCysProGlu......ArgCysAlaAlaValCys......... 195

595 ATTGAGAATGTTAAGGGCTATGAGATTGAGGACAACAAGTGTGCC 644
          |:|||||| :|||
196 ....GlyThrArgCysMetProTyrTyrVa 203

645 CCTGGTCATTTCTTTGTCTTTGCTTTATGCGTCTCTCATTGGTT 694
          ||||||| || | |||

RP   SEQUENCE FROM N.A.
RA   Shiozawa S., Konishi Y., Murayama K., Mukae N., Yamamoto F.,
RA   Hayashi S., Sato M., Shiozawa K., Tsukamoto Y.;
RT   "DR3 genome.";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB051851; BAB40663.1; -.
KW   Receptor.
SQ   SEQUENCE   417 AA;   45326 MW;   ... CRC64;

alignment_scores:
          Quality: 872.00   Length: 463
          Ratio: 1.639   Gaps: 22
Percent Similarity: 49.028   Percent Identity: 29.294

alignment_block:
US-09-525-998A-1 x Q9BY86

Align seq 1/1 to: Q9BY86   from: 1 to: 417

  43 CTCCTGGAGCTGTTGGTCGGGAATATACCCCTCAGGGCTTATTGGACTGGT   92
      |||||| ::||||| :::|||
  15 LeuLeuLeuValLeuLeuGlyAlaArgAlaGlnGly.............   26

  93 CCCTCACCTAGGGACAAGAAGAAGAAGAAGTGTGTGTCCCCAGGAA 142
      || |||:||| || ||| :|| || :::
  27 ......GlyThrArgSerProArg.........CysAspCysAlaG   37

 143 AAATATCCACCCTCAAAATAATTCGATTGTCTGTAGCCAAGTGCCACAAA 192
      :::||| :::||| |||||||| ||
  37 lyAspPheHisLysLysIleGlyLeuPheCysSerArgGlyCysProAla   53

 193 GGAACTTATTTGTACAATGGACTGC...   TCAGGAIACGGACTG 242
      ||| ||||| ||| ::|| : ||
  54 GlyHisGlyTyrLeuTyrAsnGlyLeuProCysSerGlyAsnSerThrCy   70

 243 CAGGGAGTGTGAGAGAGGTCGTCTTCACACGCTTCAGAAAAACCACCTCAGA 291
      :::||| ||||| | |||||||||
  70 sGlnValCysProG.nAspThrPheLeuAlaTrpGluAlaThrHisHisAsnS   87

 292 ..CAGTGCCCAGTGCTCCAATGCCCAAAGGCCAAAGGAAATGGCCAGGGGAG 339
      ::||| |||||| ||| || |||| ||||||
  87 erGluCysAlaArgCysSerAlaSerAspGluGlnAlaSerGlnValAla 103

 340 ATCTCTGTTGCACAGTGACAGTGGACACGGTGTGTGGCTGCAGGAAGAA 389
      ::||| || ||||||| |||||| |||||
 104 LeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysTysProGl 120

 390 CCAGTATCGGCATTATTGGAGTGAAAACTTTTCCAGTGC   429
      ||| ||||| :|| |||||||||
 120 TrpPheValGluCys........GlnValSerGlnCysValSerSers 134

 430 ..TTCAATTGCAGCCCTGCCTCAAT..GGGACCGTGCAC...   465
      ::||| ||| |||| || |||| ||||
 134 erProPheTyrCysSerGlnIleArgCysSerLeuAspGln...HisArgHis 150

 466 .....CTCTCTCCCACGAGAAACACGAACACCGTGTGCACCTGCCATGC 509
      ::|||| || ||||||||
 151 ThrArgLeuLeuCysSerArgAlaArgGlyThrAspCysCysGlyThrCysLeuPr 167

 510 AGGTTTCTTTCTAAGAGAAAAACGAGTGTGTTCTCGT   546
      |||||| |||||||||
 167 oGlyProGlyHisHisGlyAspCysTyrCysValSerCysSerProSerThr 194

 547 ..AGTAACTGTAAGAAAAAGCCTGGAGTGCACGAAGTGTGCCTACCCCAG 594
      ::|||| |||
 184 erGluSerProProGl........ArgCysAlaAlaValCys... 199

 595 ATTGAGAGAATGTAAGGCACTGGCACTCAGGGAGACTCAGGCGACAGTGTGCC 644
      :::||| |||||||| ||||
 196 ......GlyTrpArgGlnMetPhePheTrpProVa 203

 645 CCTGGTGTATTTCTTGGGCTTTGGGCTTTGTCTTTATCACTCTCTTCATTGGTT 694

```
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE-98113360; PubMed-9446802;
RA   Warzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B.,
RA   Salles G.;
RT   "A new death receptor 3 isoform. expression in human lymphoid cell
RT   lines and non-Hodgkin's lymphomas.";
RL   Biochem Biophys Res Commun 242; 376-379(1998).
DR   EMBL; AF026070; AAC49556.1; -.
DR   HSSP; P19438; INCF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS00652; TNFR_NFR-1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ   SEQUENCE   426 AA;  45959 MW;  371AA7F6AD23C16 CRC64,
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alignment_scores:
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        Quality:  362.50          Length:     471
        Ratio:    1.611           Gaps:        21
Percent Similarity: 47.77%    Percent Identity: 28.025
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alignment_block:
US-09-525-998A-1 x O14865

Align seq 1/1 to: O14865   from: 1 to: 426

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1311 CAGGAGCGGGCTT 1323
     ::::::| |||
 418 uArgSerArgLeu 422

seq_name: sp_human:000280

seq_documentation_block:
ID   000280       PRELIMINARY;       PRT;    380 AA.
AC   000280;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 9.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E.teleostomi.
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9272273; PubMed=9114039;
RA   Screaton G.P., Xu X.N., Olsen A.L., Cowper A.E., Tac R.,
RA   McMichael A.J., Bell J.I.;
RT   "LARD: a new lymphoid-specific death domain containing receptor
RT   regulated by alternative pre-mRNA splicing.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
DR   EMBL; U94510; AAC51315.1; -.
DR   HSSP; P19438; 1EXT.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00017; DEATH_DOMAIN; 1.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS00050; TNFR_NGFR_2; 1.
SQ   SEQUENCE 380 AA;  41192 MW;  ED19D586AD0947D7 CRC64.

alignment_scores:
          Quality:   354.50        Length:     461
          Ratio:     1.688         Gaps:        21
Percent Similarity: 45.553     Percent Identity: 27.115

alignment_block:
US-09-525-998A-1 x 000280

Align seq 1/1 to: 000280    from: 1 to: 380

  43 CTCCTGGAGCTGTTGGTGGAATATACCCCCAGGGGTTATTGGACTGGT 92
     ||||||      || ::|||                           :
  15 LeuLeuLeuVallLeuLeuGlyAlaArgAlaGlnGly........... 26

  93 CCCTCACCTCAGGGGAGCAGCAGCAGACAGATAGTGTGTGTCCCAACCAA 142
     :::  ||::||| |||     ::|||      :: :::CysAspCysAlaG 37
  27 ........GlyThrArgSerProArg.......... 

 143 AAIATAICCACCCCICAAAAIAAIICGAIIGCIGIACCAAGIGCCACAAA 192
     ::||| ||||:::::|||:||| ||| |||||||| |
  37 lyAspPheHisLysHisGlyLeuPheCysCysArgClyCysProAla 53

 193 GGAACTATTIGIACAAIGAITGTGATAGGCCCGGGGTAGGAIAGGAGACIC 242
     ||| |||:::|| |||::||||: :|:||  :::|||||
  54 GlyHisTyrLeuLysAlaProCysThrGluProCysGlyAsnSerThrCy 70

 243 CAGGGAGICIGAGAGCGGGCICCTTCACCGGTICAGAAAAACCACCTCAGA 241
     ::||| |||::|| ||| |||  || |||||||
  70 sLeuValCysProGlnAspThrPheLeuAlaTrpGluAspGluHisHisAsns 87

 292 ..CACTGGCCTCAGCTGICCAAAIGCCGAAAGCAAAIGGGICAGGTCGAG 339
     :::||| ||| |||       |::|||||| |||::||||||
 303 sPheAlaValProAlaArgArgIleGlySerIleValArgIleLeuGlu 319
```

```
 87 crGluCysAlaArgCysGlnAlaCysAspCluGluCysAlaAscGlnGlnValAla 103

340 AICTICIIIGACAGGACCGGCAGCA CGTGTGTGGCCTGAGGAAGAA 489
    :::::::::|| ::::||||| |::::|:::
104 LeuGlnAspCysSerAlaValAlaAspThrArgCysSerCysLysProGly 120

390 CCAGTACCGSCATTATIGGAGGTGAAAACTTTCCAGTGG....... 424
    :::: |||     |||||
120 rTrpPheValProGlu................GlnValSerGlnCysValSerGlnArgIle 134

440 ....TTCAATTGCACCTGCTGCCTCAAT...GGGACCGGGAC.......... 465
    ....GlyProPheCysProCysCysAspClyAspClyAspClyHisSerArgHis 150
134 crProPheArgCysGlnProCysGlyGluAspGlyAlaCysHisSerArgHis 150

465 ..........GlyIlc GluAsnAAA AaAvArGGIGTGCA IluGTAlgc 565
    ::::   ::::::::
151 ThrArgAspGluCysArgAlaIluAspAspCysProLeuPheSerLeuFr 167

510 AGGTTGTTCTAAAGAGAAAACGAGCIGTGCTCCTCT 546
    ||||||| |:::|||||||||:
167 GGlyPheLeuArgHisProAspCysGlyCysGlyThrSerThrL 184

547 ..AGTAACTGTNAGNAGAGCIGGAAGIIG AGAAGIIAcc IAcc AG 594
    :::||| ::::||||||||  ||
184 cnGlyGlySerCysProGlu.....ArgCysAlaAlaValCys...GlyTrp 197

595 ATTGAGAATGTTAAGGGGCACTGAG 618
    |||| ||||||||
198 ArgGlnAsnGlnAlaGlyMetGluAlaGlyMetGluAlaLeuThrProProAlaThrHi 214

619 ........CACICAGGCACCACAGIGIGTIG CAGGIGGCAITT 655
    ::::::|| ||||||||:
214 sLeuSerProGluAspSerAlaHisThrLeuLeuAlaPro........ 227

656 TGITTGGCICTTGCTTTTATCCCTGCTCTTCATTGGTTTAATGTATCGC 705
    ::|||| |||
227 ............ 227

706 IAAAAAGGIGAAAGGAAGGICGIAIGAGGCIIAIIGIGIGAAAIGGAC 755
    ::::::
227 ............ 227

227 ............ 227

756 AGCTGAAAAAGAGGGAGCTTGAAGGAACIACIATAAGCTCGGGCCC 805
    ::::|||||| |||||   ||
228 rProAspProArg....GluLysHisCysHisValSerThrVal...ValSer 241

806 CAAACCCAAGTIG AGIGC A ICGAGGIICACCCGCA Iser IIC 855
    |||   ::::|
241 LyAsn.......SerTrpThrProGlyTyrProGluTy....... 251

856 AGTCCCGIGCCAGIICCAGGIICAG ICAGCIC AGGAIAIAGCCCGG 905
    :::::::
252 ............GluGluAl 254

906 CGACICGCCAANITTCGG............GCICCCCCGTAGAGAGG 940
    ||||||||:                ||
254 aLeuCysProGlnValThrTrpSerTrpAspGlnLeuProSerAlaAlaL 271

941 TGGCAGCACCCTAICAGGGGGGCIGACCCCAIICCTIGAGACGGCCCTCGCC 990
    :::||| |||||
271 euGlyPro.......................Ala 274

991 TCCGAGCCCAICCCCAGCCCTIAGAAGGAGGAAGCAAGCCCACATTC 1040
    :::  ||||| |:::|:||:
275 AlaAlaProThrLeuSerPro.......GluSerProLeuAlaGlySe 287

1041 GCCACAGAGCCAGACCACIGAGAGCCCCGGCCCCAIAGAIGCCCGG 1090
     ::::|| ||||||||:
287 rProAlaMetMetLeuGlnProGlyPro...GlnLeuTyrAspValMetA 303

1091 AGAAGCTGCCCCGIGCCIGGAAGAATCGIGCGCGGCGTAGGTTG 1140
     ::::||||| |||::|||||
303 sPheAlaValProAlaArgArgIleGlySerIleValArgIleLeuGlu 319
```

```
1141 AGGAGCAGAGATGATGGTGAGTGCAGTGCCAAAGGAGGCTGGCTGCG 1190
     :::  |||||||  ::|::|:::|||  :::|||  :::|||
 320 ArgGluAlaGluLeuGluAlaValGluValGlyValGluGlyArg...PheAr 335

1191 CAGAGCGCAATAGCATATGCGTCAGCTCTCCTCAAT GGGAAGGCGAGAC 1240
     |||  ||||||  :|:|||  :|:|||  |||
 335 qAspGlnGlnTyrGluMetLeuLysArgTrpArgGlnGlnGlnPro.. 350

1241 CCGAGCGCCACGCTGGAGCTGCTGGAGCGGGTGCTCCCCCACACCGCCACCC 1290
     |||  |||  |||  |||  |||  |||  |||
 351 ....AlaGlyLeuGlyAlaValTyrAlaAlaLeuGluGluArgMetGlyLeu 365

1291 CTGGCTGCTGAGCACATGGAGGAGCTT 1323
     ||||||  :::  |||||||  ||||||
 366 AspGlyCysValGluAspArgGlyArgLeu 376
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seq_name: sp_human:O00279

seq_documentation_block:
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ID  O00279      PRELIMINARY;      PRT;     372 AA.
AC  O00279;
DT  01-JUL-1997 (TrEMBLrel. 04, Created)
DT  01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT  01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE  LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 8 (LYMPHOCYTE ASSOCIATED
DE  RECEPTOR OF DEATH 5)
OS  Homo sapiens (Human)
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Screaton G., Xu X.N., Olsen A., Cowper A., Tan R., McMichael A.,
RA  Bell J.;
RL  Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; U94509; AAC51314.1; -.
DR  EMBL; U94506; AAC51311.1; -.
DR  HSSP; P19438; 1EXT.
DR  InterPro; IPR000488; Death.
DR  InterPro; IPR000561; EGF-like.
DR  InterPro; IPR001368; TNFR_Cs6.
DR  Pfam; PF00541; death; 1.
DR  SMART; SM00005; DEATH; 1.
DR  SMART; SM00208; TNFR; 1.
DR  PROSITE; PS50017; DEATH_DOMAIN; 1.
DR  PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR  PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
KW  Alternative splicing.
SQ  SEQUENCE 372 AA; 40391 MW; D4F87353AB7F40F6 CRC64;
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alignment_scores:
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        Quality:  283.50      Length:   397
        Ratio:      1.477      Gaps:      20
Percent Similarity:  48.363   Percent Identity:  27.456
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alignment_block:
US-09-525-998A-1 x O00279

Align seq 1/1 to: O00279   from: 1 to: 372

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238 GATTGCAGCCAGGCAGCTGTGCGAGCGCGCTGCGTGCCACGACTTCAGAAAACCACCT 287
    ||||||  |||  :::  |||
 34 AspCys.................................AlaGlyAspPheHisLys 41

288 CAGACACTGCTAGTTGTCTCCAAATGGAAATGGGAAGGAAAATGGGTCAGGTGG 337
    |||  ||  |||  |||  ||||||  ||||||  ::::||
 41 sLysIleGlyLeuPheCysCysArgGlyCysValTrcAlaAlaSerGlnValA 58

338 AGATCTCTTCTGCACACTGCAGACAACCCGTGGTGGCCTGCAGGAAC 387
    :::||||||  :::  |||  ||||||  |||||||
 58 laLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysPro 74
```

```
388 AACAGTATGGGATTATTGGATGTGAAAACCTTTCCAGTGC 429
      |||||||      :||:
 75 GlyTrpPheValGluLys      GlnValSerGlnCysValSerSe 88

430 TTCAATTGCAGCTCTGTCTCAAT GGGAAGGCGAC 465
    |||  |||  :::  |||
 88 rSerProPheTyrCysGluProCysLeuAspCysGlyAlaLeuGluHisArgH 105

466 CCTCCTGCCAGGAGAAACAACACCCTGTGCCACCTGCCAT 507
        |||  |||  ||||||  ||||||
105 1sThrArgLeuLeuCysSerArgArgAspThrCysGlyThrCysLeu 121

508 GCAAGTTCTTTTAAGAAAAGAGTGTGTGTGT 546
    ||||||  ||||||  |||||||
122 ProCysPheTyrGluHisGlyCysValSerProHisSerTh 138

547 AGTAACTGTAAGAAAAGTTGGAGTGTAAAGTGTGCGTAGGC 592
      :::|||  |||||||  ||||||
138 rLeuGlySerCysProGlu      ArgCysAlaAlaValLys 150

593 AGATTGAGAATGTTAAGGGCAGTCAGGACTCAGGCACCACAGTCGTCTG 642
      :::||||||  |||  :::||
151 .           GlyTrpArgGlnMetPheTrp 157

643 CCCTGGTCATTTCTTTGCTTTTATCCCCTTTTCATTGG 692
      ||||||  :::  ||||||
158 ValGlnValIleLeuLeuAlaGlyVleuValProLeuLeuLeuGlyAlaTh 174

693 TTTAATGTATGTTACTAACGG TGGAAGTGTAAGTGTTACTCCATTG 739
    |||  |||  |||  |||
174 rLeuThrTyrThrTyrArgHisCysTrpProHisLys 186

740 TTTGTGGGAAATCGACACCTGAAAAGAGGGGGAGCTTGAAGGAACTACT 789
    |||  :::  |||  |||
187 .......ProLeuValThrAlaAspGluAlaGlyMetGluAlaAlaLeuThr 200

790 ACTAAGCC. CTGGCCCAAACCCAAGTTCAGTCCGCCACTCC 830
    |||  :::  |||  |||  |||
201 ProProThrAlaThrHisLeuSerProLeuAspSer 212

831 AGGCTTCACCGCACTGGCTTCAGTCGTCGGGACCAGTTCCACCTTCA 880
    ||||||  :::  |||  |||
213 .......AlaHisThrLeuLeuAlaProProAspSerSerGlnLysIleC 227

881 CCTCC.      AGTGCCACCTATACCCCGGCGGAC 909
    |||||||      :::  ||||||||
227 ysThrValGlnLeuValGlyAsnSerTrpThrProGlyTyrProGluThr 243

910           TGTCCCAACTTTGCG      GTTCCCC 942
           ||||||  |||||||      |||
244 GlnGluAlaLeuCysProGlnValThrTrpSerCysAspGlnLeuProSe 260

943 CAGAGAGGAGACACCTATCAGGGGTGGTACAACCTTGGGACAG 982
    |||  |||  :::  ||  |||||||
260 rArgAlaAlaLeuGlyPro 265

983 CCCTGGCTCCTGACCCGAACCCAACCCCTTCAGAAGTGGGAGGACAGC 1032
    |||  :::  |||  |||
266 ..AlaAlaAlaProThrLeuSerPro 276

1033 GCCCACAAGGCACAGACCTAGACACTAATGAGACGGGGACGGCTGTAGGC 1082
     ||||||  :::  |||  |||||||
277 AlaGlySerProAlaMetMetLeuLeuCysInProGlyTyrPro...GlnLeuCysTyrAs 292

1083 CGTTGGTGAAGAATGGGGCAGTTTGGTTCTGGGAGGAGAATGTCGCGGCGG 1132
     :::  ||||||  |||  |||||||||
292 pValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrL 309

1133 TAGCCCCAGGCCACCACACAACACCACCATCGCCGCGCTGCAGGAAC 1182
     :::||||||  :::  |||||||  ||||||
309 euGlyLeuArgHisAlaAspThrGluAlaValGluValGlyValGluGlyArg 325
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seq_name: sp_vertebrate:Q9PVD4

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seq_documentation_block:
ID  Q9PVD4            PRELIMINARY;       PRT;    387 AA.
AC  Q9PVD4;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DT  01-JUN-2001 (TrEMBLrel. 17, last annotation update)
DE  P75-LIKE TRANSMEMRPANF PROTFIN FULLBACK
OS  Xenopus laevis (African clawed frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC  Xenopodinae; Xenopus.
OX  NCBI_TaxID=8355;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Dick E., Sun B.I., Collins-Racie L., LaVallie E., Sive H.L.;
RT  "Identification and Characterization of fullback, a Novel Posteriorly-
RT  Expressed Xenopus Gene.";
RL  Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; AF131890; AAD54072.1; -.
DR  HSSP; P07174; 1NGR.
DR  InterPro; IPR001683. Copper_list.
DR  InterPro; IPR000488; Death.
DR  InterPro; IPR001368; TNFR_c6.
DR  Pfam; PF00531; death; 1.
DR  Pfam; PF00020; TNFR_c6; 4.
DR  SMART; SM00412; CuFIST; 1.
DR  SMART; SM00005; DEATH; 1.
DR  SMART; SM00208; TNFR; 4.
DR  PROSITE; PS50017; DEATH_DOMAIN; 1.
DR  PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_3.
DR  PROSITE; PS50050; TNFR_NGFR_2; 4.
KW  Transmembrane.
SQ  SEQUENCE   387 AA;   42066 MW;  1A386A239C7C8A82 CRC64;
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alignment_scores:
      Quality:     233.00          Length:      464
      Ratio:        1.064          Gaps:         25
Percent Similarity:  47.198    Percent Identity:  22.629
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alignment_block:
US-09-525-998A-1 x Q9PVD4

Align seq 1/1   to: Q9PVD4   from: 1   to: 387
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Align seq 1/1  to: Q9Z0W1  from:  1  to: 417

 22 GACCTCGTGCCAGCAGAAACAGCAGACACCGTGGGC.......               AAGTGCGCCGTCCGTTGGGC........ 1110
    ||| |||   |||:||::||||| ||||:|||||                        |||:||||
  2 AspArgLeuArgLeuLeuLeuLeuLeuLeuLeuLeuLeuGlyValSerPh  18    288 alysIleGluProLysLeuTyrIleAsnLeuProProHisLysGlnSerG 305

 72 TCAGGATTATTGATTCGATCATAGGGACAGGAAAGAGGAG 121                                    TGAAGGAA 1119
    :::|||||  ||:||::|:||| ::|||:||||                                               ||:||:
 18 cGlyGlyAla............................... 22    1111

122 ATAGTGCGTCCCAGGAAAATATATCACCCTCAAAATAATTCGATT 171   1120 TTCGTGTGGGCCCAGGGTGAGCAGCATGCCAGAGCCAGAGACCGGGAGTT 1169
    |||||||   ||| ||||||                               |||::| |||||| |||||| :||
 22 rsGluThrCysSerThrGlyMetTyrThrHis........SerGlyGlu 35   322 LeuAlaSerLeuLeuGlyTyrGluGluThrIleAspThrPhe 336

172 TGCTGTACCAAGCCCACAAAAGCGACCTACTGCTACAACGTCCCAGG 221   1170 GCAGAAGGCCGTTTGTGAGAAGGAATGACGGCGGAAGGGAAGGTGGCGAGCT 1219
    ||||| |||  ||| |||||| ||||||  ||| |||||                 ::: ||| ||| |||||| ||||
 36 CysCysLysAlaCysAsnLeuGlyGluValAlaGlnProCys...Gl 51   337 .......GlyArgGly...GluAspProValHisThrLeuLeuThrAsp 350

222 CCCGGGGCCAGGATACCGGACTTCAGGAGTT...GAGAGCGGCTTCCTTCA 268   1220 GCAGAAGGCGGTTGTTGATGATGATCTTGAGATCAGAACTAGCAT 1269
    ||||| ||| ||| ||| |||||| |||                          ::: ||||| |||||||||
 51 yAlaAsnGln...ThrValCysGluProCysLeuGluAspSerValThrPheS 67   350 rp.......SerSerLysGluSerSerThrLeuGluValLeuCysAla 363

269 CCGGCTTCAGAAAACCACCTCAGACACTGCCTGCCTCAGCTGCTCCAAATGCCGA 318   1270 GTGCTCCCGGACATGGACCTGCTGGCCTGGGCTGCCTGGAGGACATC 1311
    :::|||  ||||||  |||||||  |||  |||||| |||||  |||                ::||||    ||||||
 67 erAspValSerAlaThrGluProCysLysProCysThrGluGlyCys... 82   364 AlaLeuValAsnMetGluArgAlaAspValValGluGluAsnLeu 377
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seq_name: sp_rodent:Q9Z0W1

alignment_scores:
      Quality: 240.00   Length: 560
      Ratio: 1.018   Gaps: 30
Percent Similarity: 45.200   Percent Identity: 24.000

alignment_block:
US-09-525-998A-1 x Q9Z0W1

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DR   Pfam: PF00531; death. 1.
DR   Pfam: PF00020; TNFR_c6; 2.
DR   SMART: SM00005; DEATH; 1.
DR   SMART: SM00208; TNFR; 2.
DR   PROSITE: PS00198; 4FE4S_FERREDOXIN; UNKNOWN 1.
DR   PROSITE: PS50017; DEATH_DOMAIN; 1.
DR   PROSITE: PS00652; RIBOSOMAL_S2_1; UNKNOWN 1.
DR   PROSITE: PS00962; TNFR_NGFR_1; UNKNOWN 1.
DR   PROSITE: PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   368 AA;   41020 MW;  5701AC2A6B4F07D2 CRC64;

alignment_scores:
             Quality:   227.50          Length:      450
             Ratio:     1.155           Gaps:         19
     Percent Similarity: 44.778   Percent Identity: 24.778

alignment_block:
US-09-525-998A-1 x O57408

Align seq 1/1  to: O57408  from: 1  to: 368


40  GTGCTCCTGGGAGCTGTGGGTGGGGCAATATACCGTCAGGGGTTATTGGGACT  89
                 |||||||  |||||||   |||     :|:|||||
11  ValLeuLeuGluLeuLeuAlaLysVal........................  19

90  GGTGCCTCACCTAGGGACAGGAGGAGAGATAGTGTGTGTGCGGCAAAG 139
                 ||||||||          ||| |||  ||:
20  .......HisLeuGlySerAlaAlaAlaVallysSerArgAlaVallysSS  44

140 GAAAATATATGCAGTCAAAATAATGCATTGTGCATGCAATGGCAC 189
                 ||||||  ||||      :||     ::|    LysCysCysPro 47
34  erAspValLeuGlyProAspProTyrSer................

190 AAAGGAACCTACTTGTACAGACTGTCCAGGCGCCGGGGTAGGATAGGA 239
                 |||||| |||| |||||      |||||     SerSerAr 58
48  MetGlyThrTyrLeuAlaAsnAsp....................

240 CTGCAGGGAGTGGAGAGCGGCTTCAGCGCCTTCAGAAAAACCCCA 289
                 ||| |||||||||     :|||||||||   |||
58  gCysLeuProCysLysLysAspGluTyrThrGlnTyrProAsnAspProHen 75

290 GACACTGCGTAGGTGTGCAAAAGCGGAAAGGAAAGAAATGGGAGGAGAAG 339
                 ||||||||||||      :|||||||     ||| GlnValGlu 89
75  rolysCysLeuGlyCysArgThrCysArgGluAsp........

340 AATCTCTTCTGCACAGTGGACGCGGACACCGTGTGCTGCACGAGAAGAA 389
                 :::|||   |||      :|||||||| PheCysLeuAspHisProCysSer 104
90  ValSerProCysAsnSerThrArgAsnIhrArgCysSerAlaCysSerS....

390 CCAGTACCCCATTATTGAGAGTGAAAAACCTTCCAGGGTCCCAATTGGCA 439
                                                      AAAAATCC 104
104

446 GGCTCAGCTAAAGGAGGTCGAGGTCGGCTCCTGGGAAGAAAAGAAAC AGAAC 489
                 :|||||||     :|||||||||||||||||     AlaAlpAsnAspAsnAsn 107
105 .........AsnGlyThr.............

440 ACCGTGTGCACCTGCCATGCAGGGTTCTTTGTAAGAGAAAAGCAGGGGGT 489
                                                     :|:::
108 ................PheCysLeuAspHisProCysSerAlaCysSerS 116

540 CTCCCTGTAGTAACTGTAAG.............. AAAAGTCC 445
                                                 :::|||
116 uMetGlyGluLysCysCysGluHisArgTyrSerAlaTyrSerValArgGlnLeuA 133

565 TGAATGGCAGCAA..................TAGGCCTGAGGAGGTAGAATCAACAAT 485
                 ||||||||||       |||||
133 LaAlaCysIleGlnSerAspLeuAsnArgCysGlyProAlaLeuAspAspAsn 149

604 GTTAAGGCACTGCAAGACTGCAGGCTAGCACAGTG......... CTGTGGCCGCC 447
                 ||||      :||||
150 SerSerSerPheThrThrGlyIleIleIleSerTrpValLeuProVal 166
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seq_name: sp_vertebrate:O57408

seq_documentation_block:
ID   O57408        PRELIMINARY;      PRT;    368 AA.
AC   O57408;
DT   01-JUN-1998 (TREMBLrel. 06, Created)
DT   01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT   01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE   SUBGROUP E ALV RECEPTOR.
OS   Meleagris gallopavo (Common turkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX   NCBI_TaxID=9103;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Adkins H.B., Brojatsch J., Naughton J., Rolls M.M., Pesola J.M.,
RA   Young J.A.T.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF006002; AAB91987.1; -.
DR   HSSP; P19438; 1EXT.
DR   InterPro; IPR001450; 4FE4S_ferrdxin.
DR   InterPro; IPR000488; death.
DR   InterPro; IPR001855; Ribosomal_S2.
DR   InterPro; IPR001368; TNFR_c6.
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733  TCCATTGTTGTGGGAAATGCAACCTGAAAAAGAGGGGAGCTTGAGG 782
271  ..........CysCysProAsnLys.............GlnCl 277

783  AACTACTACTAAGCCCTGGCCCAAACCAAGCTCAGTCCCACTCCAG 832
277  yAlaAsnSerArgProValArgGluThrPro.....ProProGln 291

833  GC........TTCACCCCAGCCTGGCTCAGTGCCGTCCCCAGGCGCACC 876
291  lyGlyLysLeuHisSerAspSerGlyIleSer...ValAspSerGlnSer 306

877  TTCACCTAAGCTCCACTATACCCCGGCATGATCTCCTAATTTGAAGC 926
307  IleHisAspGlnIleThrHisThr.............. 314

927  TCCGGAGAAAGGGACAACTATCAAGGGGTGACCATCCTTG 976
315  ...GlnThrAlaSerAlaGlnAlaAlaLysGly....AspGlyAsnLeuT 329

977  CCGACGCCCTCCCCCGATCCATCCGCCAACGCCTTCAGCAAGTGGGAG 1026
329  yrSerSerLeu................ProLeuThrLysArgGlu 338

1027 GACAGCATCAAGGTTAAGCTTAAATAATAGTGAAAATCCAGCACGCT 1076
339  Glu..ValGluGlySerGluAsnGlyAspThr........ 348

1077 GTACGGCGGTGGTGGAAAACATGCCCCGTTGGCGGTGGGAATTCGTGC 1126
349  ...............TrpArgHisLeuAlaG 354

1127 GGCGGCCTAGGGCTAGGCCACCAGAATCGATCGGCTCGGAGCCTGCAAAC 1176
354  lyGluLeuGlyTyrGlnProGluHisIleAsp......SerPheThrHis 368

1177 GGGGGCTGTGCTGGAGGCGCAATAGAGCATGCTGGCATGGAGCG 1226
369  GluAlaCysProValArgAla........LeuLeuAlaSerTrpGlyAl 382

1227 GGGCAGAGGTGGCCGATTAAGCTTGCATGCGTTGGAGTGGCTGGT 1275
382  aGlnAsp..........SerAlaThrLeuAspAlaLeuLeuAlaAlaLeuA 396

1277 CCGGACATGGACCTTGGGGTGAGCAAGAAGCAGGGGGTTTGC 1326
396  rqArqIleGln..........ArqAlaAspIleValGluSerLeuCys 408
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RA   Bobe J., Goetz F W.;
RT   "Molecular cloning and expression of a TNF receptor and two TNF
RT   ligands in the fish ovary.";
RL   Comp. Biochem. Physiol. B, Comp. Biochem 0-0 0(2000).
DR   EMBL; AF25004?; AAC24365.1; -.
DR   InterPro; IPR000345; Cytc_heme_bind.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   438 AA; 49103 MW; B7E531_BRBGBCH4 CRC64;

alignment_scores:
     Quality: 225.00   Length: 512
     Ratio: 1.037   Gaps: 24
     Percent Similarity: 42.383   Percent Identity: 21.680

alignment_block:
  US-09-525-99RA-1 x Q9DFV0

Align seg 1/1 to: Q9DFV0   from: 1 to: 438

1   ATGGGCCTCTTCCACCGTGCCTGCTCCCACCTGGTGCTGCTCCCACTGGTGGTCCTCTGGA 50
     ||| || || | || || || | | |||| ||| |||||
1   MetAspLysSerGluAlaMetLysValCysMetAlaLeuVallIlePheSe 17

51   GCTGTGGTGGGGAATATACCCTCAGGGGTTATTGGACTGGTCCCCTCACC 100
     ||| :::||||||||
17   rLeuAlaLeuValGlyHisGlyAlaAlaGluLeuGlyValSerAlaAspH 34

101 TAGGGGAYAGGGAGAAGAGAGATAGTGGTGTCTCCCAAGGA...AAATAT 147
     ||| ||| ||| ||| ::||::
34   isGlnAsnArgThrAlaArgGlnMetThrCysLeuGluAsnHisGluIyr 50

148 ATCCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAAC 197
     |||||| ::||||||||
51   ProHis.........AsnGlyPheCysCysLysAsnCysGluAlaGlyTh 64

198 CTACTTGTACAATGACTGTCCAGGCCCGGGCACGATACCGGACTGCAGGG 247
     |||| :::||||||||||||||||
64   rTyrValLysGluLysCysThrSerGlyGlyHisValMetGlyLysCysSerP 81

248 AGTGTGAGAAGGTCTTCAACGGTTCAGAAAAAGAACACTGC 297
     :: |||||| ||||||||
81   roCysGluLysCysGlyThrTyrAlaGluHisProHisCysMetCysGluCysCys 97

298 CTCAGGCTGGTCCAAATGCCGAAAAGGAAATGGGTCAGGTGGAGAATCTCTTC 347
     |||||| ||||||||||||||||||
98   LeuGlnCysHisCysHisArgArgGln 107

348 TTGGCACAGTGGACGGGGACCACGGTGTGTGCGTGCGAGAAGAACCAGTACC 397
     ||||||||||||||||||

398 GGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATGCAGCCTGC 447
     |||

448 CTCAATGGGACGGGTGCACCTCGTGCTCCAGGACGAAACAGAACACCGTGTG 497
     ||||||

498 CACCTGCCATGCCAGCTTTCTTTGTCAAGAGAAAACGAG 535
     ||||||

546 GTGTCTGGTAGTAATGTAGAAGAAAAGTTGAAGTGCAGAATTGTGC 585

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390  yrAspLeuLeuArgValTrpMetGlnLysGluGlyLeuArg... AlaAsn 405

1252 CTGGAGCTGCTGGGACGCGTGCTGGCGGACATGGAC 1287

406  IleAsnThrLeuGlnAspLeuAlaGluLeuAspLeuGluAsp 417


seq_name: sp_human:014866


seq_documentation_block;
ID  014866        PRELIMINARY;         PRT;    277 AA.
AC  014866;
DT  01-JAN-1998 (TrEMBLrel. 05, Created)
DT  01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT  01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE  SOLUBLE DEATH RECEPTOR 3 BETA.
GN  DR3.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Warzocha K., Ribeiro P., Renard N., Charlot C., Coiffier B.,
RA  Salles G.;
RL  Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; AF02xxxx; AAxx2288.1; -.
DR  HSSP; P19438; 1NCF.
DR  InterPro; IPR000561; EGF-like.
DR  InterPro; IPR001368; TNFR_c4.
DR  Pfam; PF00020; TNFR_c6; 2.
DR  SMART; SM00208; TNFR; 2.
DR  PROSITE; PS00652; TNFR_NGFR_1; 2.
DR  PROSITE; PS00653; TNFR_NGFR_2; 1.
SO  SEQUENCE  277 AA;  29311 MW;  3D19F3E847HFCxxx CRC64;


alignment_scores:
        Quality:         219.50          Length:      347
        Ratio:           1.546           Gaps:        14
Percent Similarity:   42.136       Percent Identity:   24.429

alignment_block:
US-09-525-998A-1 x 014866

Align seq 1/2  to  014866  from: 1  to: 277
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RP   SEQUENCE FROM N.A.
RA   Screaton G.R., Mongkolsapaya J., Xu X., Cowper A.E., McMichael A.J.,
RA   Bell A.J.;
RL   Curr. Biol. 0:0-0(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Schneider P., Bodmer J.-L., Thome M., Hofler N., Holmann K.,
RA   Tschopp J.;
RL   FEBS Lett. 0:0-0(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yuasa Y.;
RT   "Genomic structure and mutation analysis of the DR5/TRAIL receptor 2
RT   gene in colorectal carcinoma.";
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF018658; AAB70578.1; -.
DR   EMBL; AF012266; AAB81185.1; -.
DR   EMBL; AB014718; BAA33723.1; -.
DR   EMBL; AB014710; BAA33723.1; JOINED.
DR   EMBL; AB014711; BAA33723.1; JOINED.
DR   EMBL; AB014712; BAA33723.1; JOINED.
DR   EMBL; AB014713; BAA33723.1; JOINED.
DR   EMBL; AB014714; BAA33723.1; JOINED.
DR   EMBL; AB014715; BAA33723.1; JOINED.
DR   EMBL; AB014716; BAA33723.1; JOINED.
DR   EMBL; AB014717; BAA33723.1; JOINED.
DR   HSSP; P19438; 1NCF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   SMART; SM00005; DEATH; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NCF2; UNKNOWN_2.
DR   PROSITE; PS00650; TNFR_NGFR_2; 2.
SQ   SEQUENCE  440 AA;  47894 MW;  7E9367DF3ED24DDE CRC64;
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alignment_scores:
     Quality:   217.50          Length:     465
     Ratio:       1.021         Gaps:        22
     Percent Similarity:  45.806    Percent Identity:  23.656

alignment_block:
US-09-525-998A-1 x O15531

Align seq 1/1 to: O15531  from: 1  to: 440

  19  ...TGA.TGCTGGTGCA.........CTGATCGTCCTGAACT.TGAGGTTGGGTTGG  62
         ||| ||     :::|||           ||||||||:::
  30  ProGlyLeuArgValProLysThrLeuLeuValLeuValAlaAlaValAlaValIle  46

  63  AATATACCCTCAAGATTATTGGATGGTCCTTCAACAAGGGA'AGGGACAGGG  112
        :::                   LeuCysProProGlyHisHisLeuSerGlnAs  90
  74  Gly

 213  CTGTC.AGCCCGGGACAGGAGTGGAGGTGAGAGAGCGAC  261
         ||||                     |||||||||
  96  GlyArgAspPro...GlnSerLysLysTyrArgTyrG  101

 113  AGAAGAGAGATTAGTCGTGTCGTCCCCAAGGAAAATATATCCACCTCAAAAT  162
        ||    ||  ||||:::|||    ||||||||:::
  62  laProGlnArgValAlaProGlnInLysSerProSerGluGlu  78

 163  AATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGA  212
        |||                   LeuCysProProGlyHisHisLeuSerGlnAs  90
  79  Gly

 262  ...TCCTTCAGCGGCTTCAGAAAAACCACCTCAGACACTGCCTCAGCCGTCCTCC  309
        |||||     ||||||||:::
 101  lnAspTyrSerThrHisTrpAsnAspLeuLeuProLeuLeuLeuArgCysThr  117
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sed_name: sp_human_o15531

seq_documentation_block:
ID   O15531      PRELIMINARY;     PRT;   440 AA.
AC   O15531;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   APOPTOSIS INDUCING PROTEIN.
GN   TRICK2R OR DR5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
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310  AAAAGCGGAAAGGAAAAGGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGA  359
     :::::||    ::: |||  |||||||  ::: |||  |||||||
118  ArgCys.....AspSerGlyValGluValGluLeuSerProCysThrThrTh  132

360  CCGGGAACACGGTGTAGGATGTAAGAAAACTATAGTTGATTATTGGA  409
     :::||||||||| |||:::||||||| ::::||:|||
132  rArgAsnThrValCysGlnCysGluGlyThrPheArgGluGluAspS  149

410  GTGAAAACTTTGCAGAGCTGAATTGCAGCCTC...TGACTCAATGGG  456
     ||  :::||||   |||    ||| |||  :::||||
149  rProGluMet.......CysArgLysCysArgThrGlyCysProArgGly  163

457  ACCGTG.....................CACCTCTCTGCCAGGA  479
     ::::::                      ::  :::
164  MetValLysValGlyLysAspCysThrProTrpSerAspIleGlyCysValHi  180

480  GAAACAGAACACGGTGTGCACCTGCACTGCAGGTTCTTCTTCTAAGAGAAA  529
     :::||||                  ::||||| ::|| :::
180  GlysGluSerGly......ThrLysHisSerGlyGluAlaProAlaValG  195

530  ACAGATGTGTGTCTGTAGTAACTGTAACAAAAGTGAGTGAGTGAAAAG  579
     :::|| |||:::||| |||                ::|||||||  :::
195  luGluThrValThrSerSerProGlyThrProAlaSerProCys.....  209

580  TTGTGTCCCAGATCGCAGAATCTAAGGGCACTGAGGCACTCAGGCAC  629
     :::                      ::: |||  :::||
210  .........................SerLeuSerGlyTileIleIleGlyValTh  219

630  GAGATGTCTGTCCCGGTCAGTCAGATTCCTTCGTTTGCTTTTATCCC  679
     :::      :::||||:::||| ::|||||  :::
219  rValAlaAlaValLeuLeuValAlaValPheValCys.....LysSerL  235

680  TCCTCTCATTGGTTTAATCTACTAACTGTGAAGTGCAAGGTC  729
     ||||||                  :::|||||
235  euLeu.......................TrpLysValLeu  241

730  TACTCCATT.......GTTTGT........GCGAAATCCGCACCTGAAAAAGA  767
     ||||||          :::|||||               :::
242  ProTyrLeuLysGlyIleCysSerGlyTrGlyGlyAspProGluArg..  257

768  GGGGGAGCTTGAAGGAATAATAAACCCCTGGCCCAAAACCCAAGCT  817
     ::||||||      |||           :::|||
258  .......ValAspArgSerSerCysArgProCysAlaCysAspAsnValE  272

818  TCAGTCCC.......ACTCCAGGTTTCTATCCCCACCTGGGG  852
     ::::                      :::||
272  euAsnGlnIleValSerIleLeuLeuGlnSerThrGlnValPro  288

853  TTCAGTCCCGTGCCCAGTTCCACTCCTGGCCACCTCACCATACCCC  902
     ::||||||                  :::|||||
289  MetGlyValGlnGlyGluProAlaGlnLeuProThrGlyValAsnMetLeuSerPr  305

903  CGGTGACTGTCCCCAACTTTGCGGGTCCC  930
     ||||||      |||
305  oTyrTrpSerProHisLeuGlyGluProAlaGlyHisAlaCysArgSerGlnA  322

931  CGTAGAGAGGGTGCACACGGTGGGTGACCATGTTGGG  978
     ||||||      |||
322  rgAsnArgLeuGluValProAlaAsnGlyGly.........  332

979  ACAGCCCTGGGTCGGGAGACTGGTCAACCCTTCAACAAGGTGGGAGGA  1028
     ::::||                      :::||
333  ......................AspProThrGluThrLeuArgGlnCysPheAspAs  344

1029 CAGGGGCGACAAGGTGCACACAGTTAGACTAGATCACCGACAGTGT  1078
     ::||||                      :::||
344  rPheAla....................  346

1079 ACACGTGTGGTGGAGCATCGTGGTTGGTTGAAGCAATTCATGTGAGGG  1128
     ::||||      |||
347  ..............AspLeuValProPheAspSerTrpGluProLeuMetLArg  359

1129 CGGCTAGGGCTGAGGGACCATCGACATCGGACGTGGAGCTGGAGAACGG  1178
     ::||||                      :::||
360  laAlaProGlnGlyLysArgSerSerProSerGluGlyLeuCysProProPro  384
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               :::||||||      ::: ||||||
360  LysLeuCysThrLeuMetAspAsnGluIle.....LysValAlaGlyAsnGlu  ?75

1179 GCGGTGCTGCGGAGCGAAGTGAAATAACAGCAGGTGGAGACCTGGAGGTGGC  1228
     :::||||      |||               :::
375  AlaAlaGlyHisAlaAspThrHisTyrThrMetLeuGlyProValAshM  ?92

1229 GCACCGCCGGCCGGCGCGCCACGGCTGGAGCTGCTGGAGCTGCTGGAGCTGCTGCGGAGCCGGTGCTCCGGC  1278
     ::|||
392  ySTLr.....................GluArgIleAspAlaAlaSer  ?98

1279 GACATGGAGTGCTCAGGTCCTGAGGACATCGGAGGAGGTGGTT  1323
     ::|||||      |||
399  ValHisThrLeuHisAspAlaLeuGluGluThrLeuGlyGlnAspArgLeu  414
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seq_name: sp_human_O14763

seq_documentation_block:
ID   O14763                 PRELIMINARY;           PRT:     410 AA.
AC   O14763;
DT   01-JAN-1998 (TREMBLrel_05, Created)
DT   01-JAN-1998 (TREMBLrel_05, Last sequence update)
DE   01-JUN-2001 (TrEMBLrel_17, Last annotation update)
DE   APOPTOSIS INDUCING RECEPTOR FOR TRAIL R2.
GN   TRAILR2.
OS   Homo sapiens (Human)
OC   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
OC   Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97459925; PubMed=9311998;
RA   Walczak H., Degli Esposti M.A., Johnson R.S., Smolak P.J., Waugh J.Y.,
RA   Boiani M., Timour M.S., Gerhart M.J., Schooley K.A., Smith C.A.,
RA   Goodwin R.G., Rauch C.T.;
RT   "TRAIL-R2: a novel apoptosis mediating receptor for TRAIL.";
RL   EMBO J. 16:5386-5397(1997).
DR   EMBL; AF016849; AAC51778.1;
DR   HSSP; P19438; 1NCF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS50050; TNFR_NTR_1; 0.4  WN..
DR   PROSITE; PS50050; TNFR_NTR_2; 2.
SQ   SEQUENCE  410 AA;  47850 MW;  69408547A8B4879 CRC64;
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alignment_scores:
               Quality:    215.00            Length:      471
               Ratio:      1.014             Gaps:         22
               Percent Similarity: 41.825    Percent Identity: 34.394

alignment_block:
US-09-525-998A.1 x  O14763 ...

Align seq 1/1 to O14763 from 1 to 446

16   GTGCTGCAGCTGCTGCTGCTGCTGCTGCTGCACTGTGGCTGCTGGAGCTGCTGGGGGCAA  75
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34   ValProLysThrLeuValValLeuValValAlaAlaValLeuLeuLeuValSe  ??

66   ATACCCCTCAGGGTTATT................GGACTGGTCCC.....CATC  100
     ||||||      |||                      :::
50   rAlaGlnSerAlaLeuIleThrGluGlnGlnAspLeuGlnProGlnGluArgA  ?7

101  TAGGGGACAGGGAGGAGAGAGATAGT...............ATGTGGTGGGAA  148
     ||||||      |||
67   laAlaProGlnGlyLysArgSerSerProSerGluGlyLeuCysProPro  84
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```
331 ::::|||
    GlnGly

1005 CAAGCCCTTCAGAAGTGGAGGAGCAGGCACAAGGCACAGCTAG 1054
     ::: :::::||| ||
336 uThrLeuArgGlnCysPheAspAspPheAla............. A 346

1055 ACACTGATCACCGCCGCAGCCTGTACGCCGTGGTCGAGAACGTGCCCCCG 1104
     ::: ||||||
347 ......                    AspLeuValProPhe 351

1105 TTGCGCTGGAAGGAATTCGTGCGGCCTAGGGCTGAGGCCACCAGGAGAT 1154
     |||::::   :::||:||||||||  |||::::||||
352 AspSerTrpGluTrpGluMetArgLysLeuGlyLeuMetAspAsnGluTl 368

1155 CGATGGGTGAGGTGGAAGGTGAAGGTGGTGGAGAAGGAATACA 1204
     | :::::|||    ||:||||  ||:|||
368 e...lysValValAlaGluAlaGlyHisArgAspThrLeuTyrTl 384

1205 GCAGCTGGCGAGCACGGGAGGCGGGCACCGCGGCGGAGGCGACAGCTG 1254
     ::||||||  |||
384 hrMetLeuIleLysTrpValAsnLysThr.............. 393

1255 GAGCTGCTGGGACGCGGACGACACAGGACCAGCTGCGGGCGCGGGA 1304
     ||||||        |||  |||::::||||
394       GlyArgAspAlaSerValHisThrLeuLeuAspAlaLeuGl 407

1305 GGAGATCGAGGGAGGGTT 1323
     |   ||| |||
407 uThrLeuGlyGluArgLeu 413
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189 GGAAAATATATCCCACCCTCAAAATAATTCGCATTGCTCTACCAAGTCGCCA 188
    |||  :::|||  :::||||||  :::::
84 GlyHisHisIleSerGluSerGluAspGlyIyArg.............. 92

189 CAAAGGAACCTATTGTATAATATGTCTAAGGCTGGGGAAGGACAGATAGGG 238
    :::  :::::|| :::::::||| |||
93 ...........                               A 93

239 ACTGCAGGAGTGTGAGAGGGT...ICTTCACCGCTTCAGAAAACCAC 285
    ::|||:::: ||  |||::::||||  |||
93 spCysIleSerCysTyrCysTyrGlnAspTyrSerThrHisTrpAsnAsp 109

286 CTTCAGACACTGCCTCAGTCTGCTCCAAATGCCGAAAGGGTCAGGT 335
    |||  :::|||  |||:::|||  |||  ||||||
110 LeuLeuPheCysLeuArgCysThrArgCys.....AspSerGlyGluVa 124

336 GGAGATCTTTCTTCTGCACAGTGGACACGGGACACCGTGTGTGGCTGACAGGA 385
    :::||||  :::|||  ||||
124 lCysLeuSerProCysThrThrThrArgAsnThrValCysGlnCysGluG 141

386 AGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTCCNGTGCTTCAAT 435
    |||::::||||  :::|||||| |||
141 luGlyThrPheArgGluGluGluAspSerProGluMet....... 155

436 TGCAGCCTC....TGCCTCAATGGGACCGTG 462
    |||   |||  :::|||
156 CysArgThrSerLysProCysArgGlyMetValLysValGlyAspCysThrF 172

463 ...........CACCTCCTGCCAGAGAAACAGAACACCGGTGCACCTGCC 505
    :::::|||||| :::|||  |||  ||||
172 oTrpSerAspProGluCysIleHisLysGluSerGly......ThrLysH 187

506 ATGCAGGTTCTTCTCCAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGT 555
    ::::||||  |||||||| :::||||
187 isSerGlyGluAlaProAlaValGluGluThrSerSerProGly 203

556 AACAAAACCTGCAGTCACCGGACCTTGCCTACCCCAGATTGAGAATGT 605
    :::  :::::|||
204 ThrProAlaSerProCys            SerLe 211

606 TAAGGCACTGAGGACTTAGGGAATCTAGTGTTTGGCCCGCCGGGTCCATTT 655
    :::::||| |||::::|| |||
211 uSerGlyProGlyThrGluGlyProValLeuValAlaValLeuLeuValA 228

656 TCTTTGGTCTTGGCCTTTTATCCATCCTTCATTGGGTTAAAGGTATCGGC 705
    ::::|||  |||||||||
228 laValPheValCys....LysSerLeuLeu 236

706 TACTAAACGGTGGGAAGCTCAAGCTCTACACCCATT.......GTTGT 744
    ::::||| :::
236 ......       TrpLysValLeuProTyrLeuGlyTyrIleCysSerGl 250

745 .GGGAAATCGACACCTGAAAACAGGGGGAGCTTGAAGGAACTACTACTA 793
    :::::||| :::
250 yGlyGlyCysAspProCysArg..... ValAspArgSerSerGlnA 264

794 AGCCCCTGCCCCCAAACCCAAGCTTCAGTCCC...........ACT 828
    :::::|||::::
264 rgProGlyAlaGluAlaSerAspAsnValLeuAsnGluIleValSerIleLeuLeuGln 280

829 CCAGGCTTCACCCCACCCGCCTTCAGTCCCCCAGTTCCACCTT 878
    |||  :::
281 ProThrGlnValProGlnGlyGluMetGluValGlnGlyProAlaGluPr 297

879 CAGTCCAGTCACACTATACCCCGGTGACTTGTGCCCAATTTGCGGCTC 928
    |||::::||||||||||  :::::
297 oThrGlyValAsnMetLeuSerProGlyCysGluSerGluHisLeuLeuGluP 314

929 CC......                CGCAGAGAGTGGCACCCACCCTAT 954
    :::|||  |||:::||
314 roAlaGluAlaGluArgArgSerGluArgArgLeuLeuValProAlaAsn 330

955 CAGGGGGGGCTGACCCCATCCTTGCGACAGCGCGCGCCTTCGGACCCGACCCCATCCC 1004
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